

**5981193**

H alpha 2  
(2600 bp)

# rat alpha 2

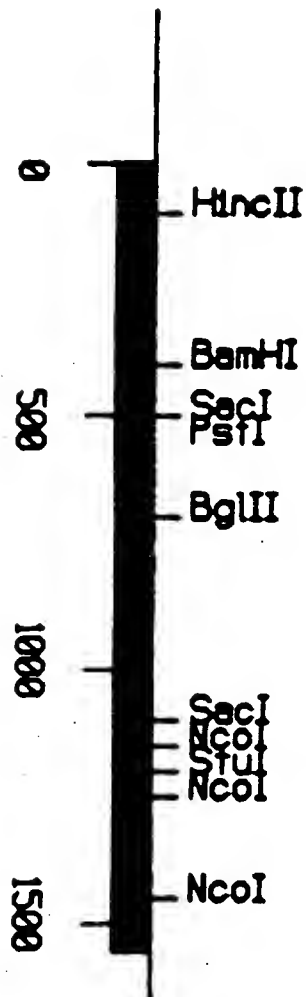
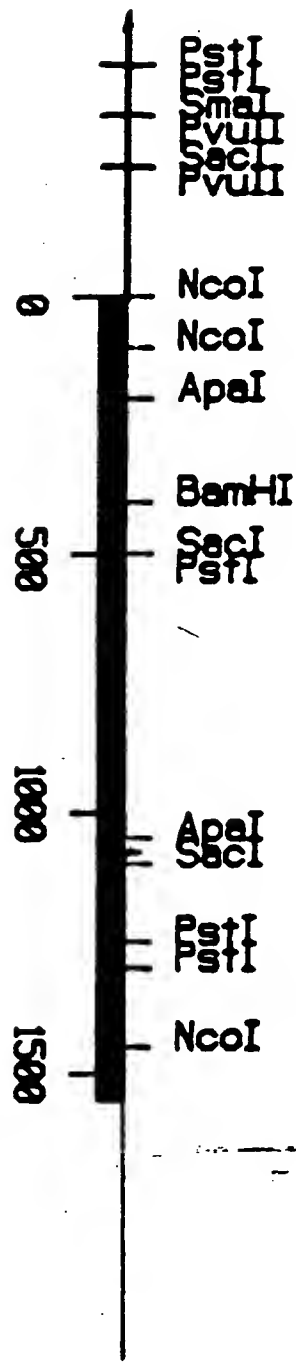


FIGURE 1

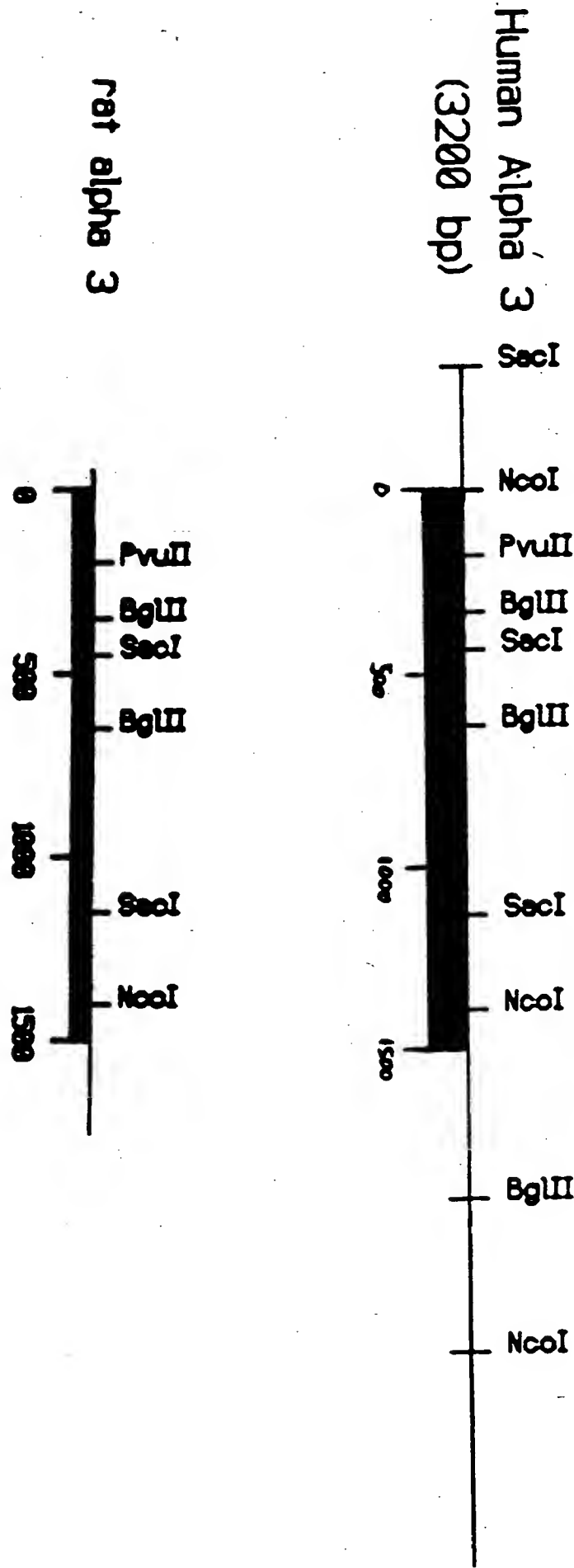


FIGURE 2

(3 of 11)

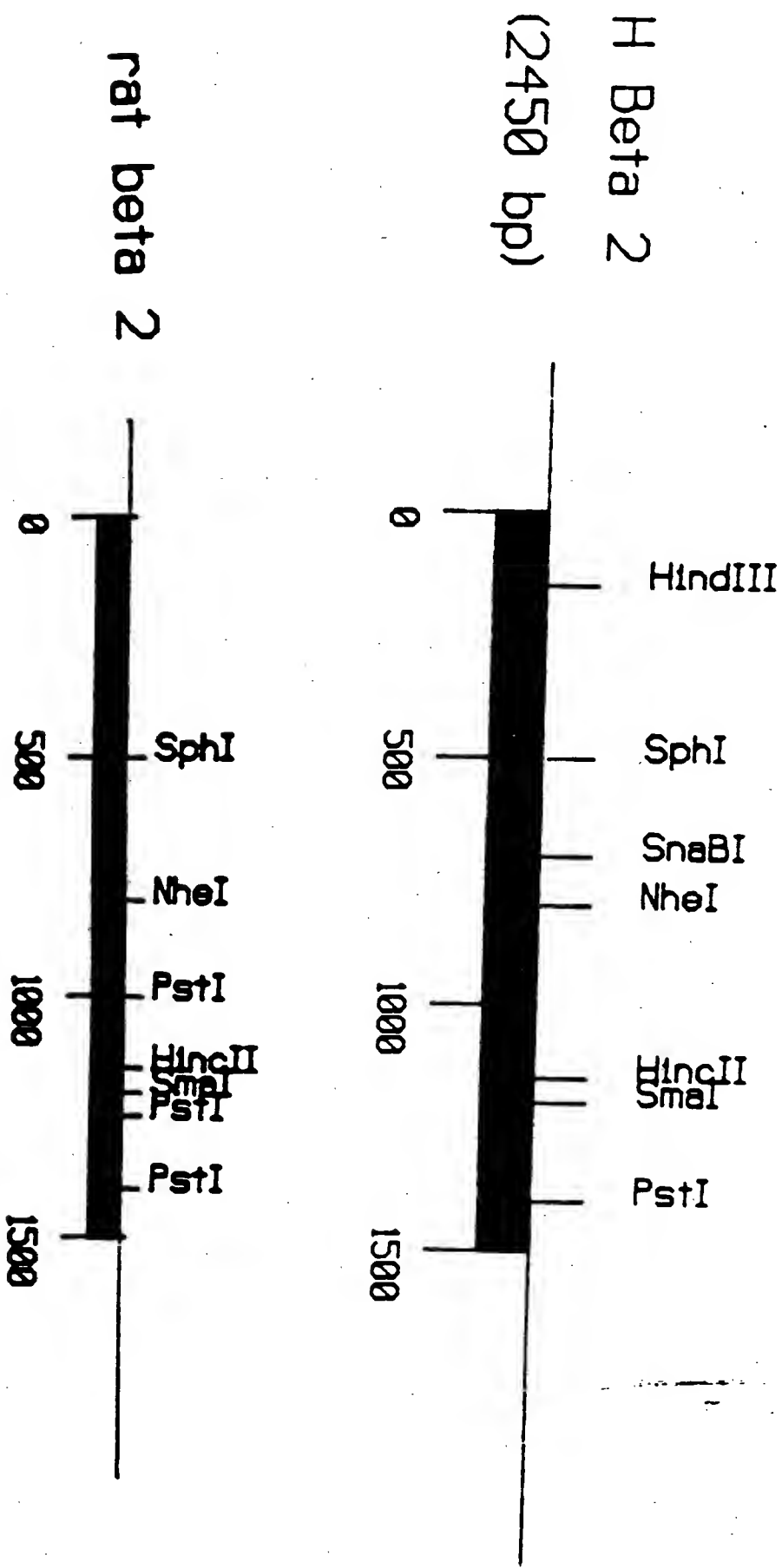


FIGURE 3

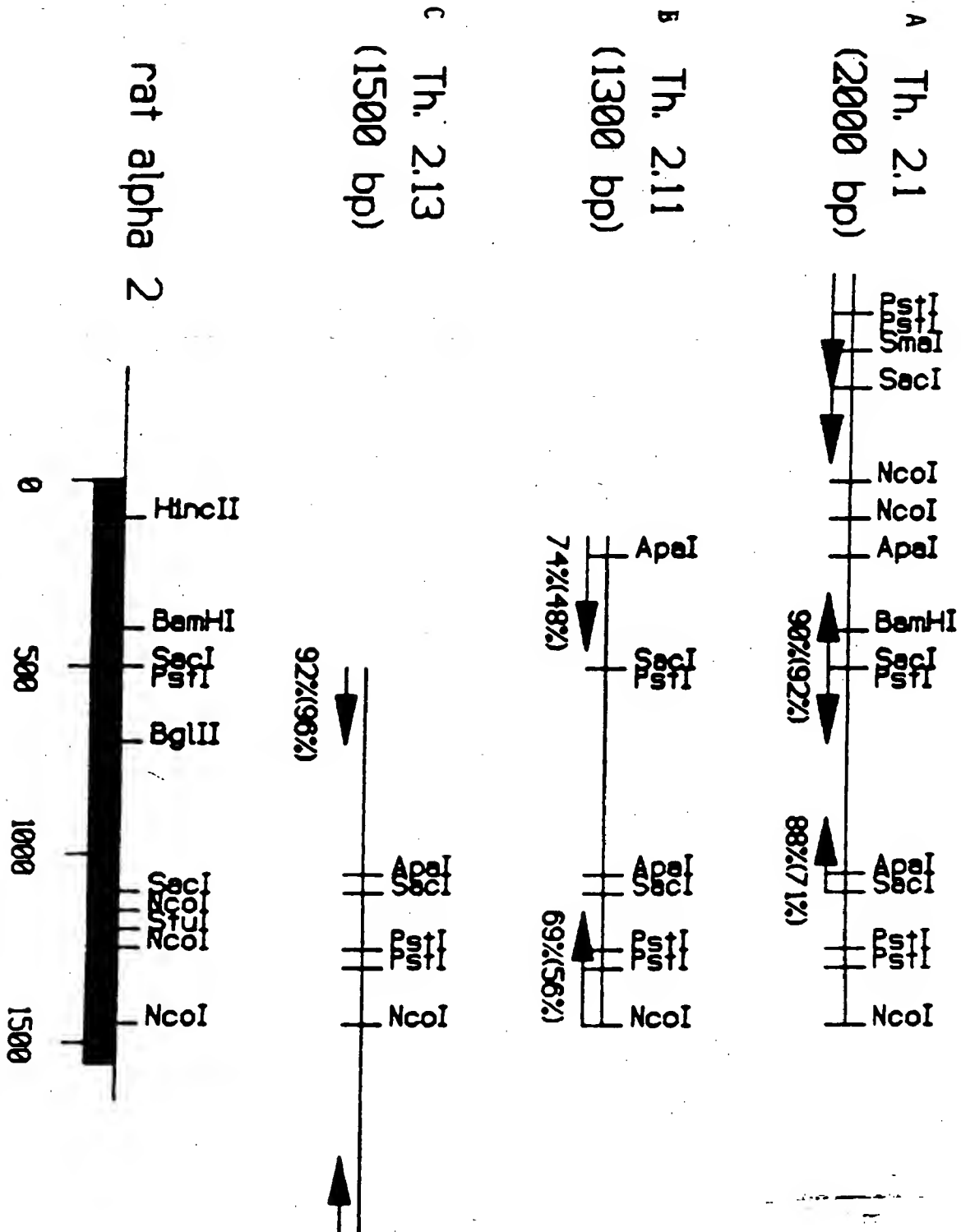


FIGURE 1

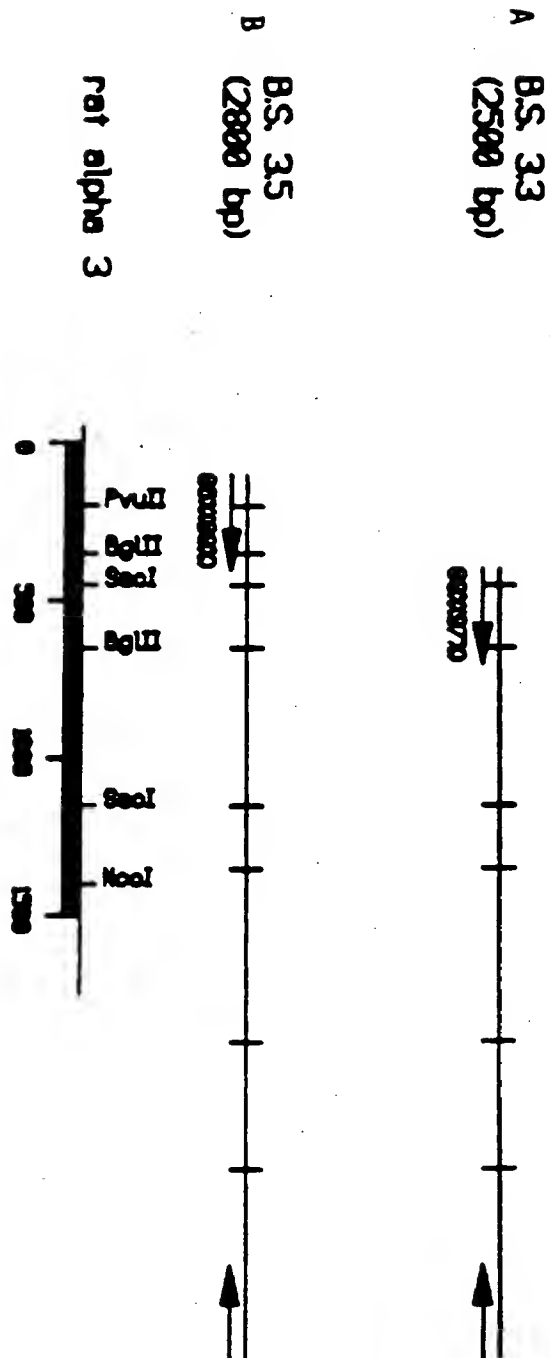


FIGURE 5



## FIGURE 6

SECTION A

```

195 .....GCTAAACAGGAGTGGAGCGACTACAACTGCGCTGGAAC 157
      II IIII IIII IIIIIII IIIIIII II
251 CCAATGTCTGGCTAAAGCAGGAATGGAATGACTACAAGCTGCGCTGGGAC 300
156 CCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGAT 107
      II IIII IIIIIII IIII II II IIIIIII IIIIIII
301 CCGCTGAGTTTGGCAATGTCACCTCCCTGCGCGTCCCTTCAGAGATGAT 350
      BaHI
106 CTGGATCCCGACATTGTTCTCTACAACAA...AAATGGGGAGTTTGCAG 60
      IIIIIII IIIIIII IIIIIII IIII IIIIIIIII IIII
351 CTGGATCCAGACATTGTCCTCTACAACAATGCAGATGGGGAGTTTGCAG 400
      59 TGACCCACATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCACTGG 10
      IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII
401 TGACCCACATGACCAAGGCTCACCTCTTCTTCACGGGCACTGTGCACTGG 450
      9 GTGCCCCC
      IIIIIII
451 GTGCCCCCA

```

SECTION B

```

1 CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACTTATG 50
      IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII IIII
501 CCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCCTGGACATATG 550
51 ACAAGGCCAAGATCGACCTGGAGCAGATGGAGCAGACTGTGGACCTGAAG 100
      IIIIIII IIIIIII IIIIIII IIII IIIIIIIII IIII
551 ACAAGGCCAAGATCGATCTGGAGCAGATGGAGAGGACAGTGGACCTGAAG 600
101 GACTACTGGGAGAGCGGCGAGTGGGCCATCGTCAATGCCACGGGCACCTA 150
      IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII
601 GACTACTGGGAGAGTGGCGAGTGGGCCATTATCAATGCCACCGGAACCTA 650
151 CAACAGCAAGAAGTACGACTGCTGCGCCGAGATCTACCCCGACGTCACT 200
      IIII IIIIIII IIIIIII IIIIIII IIIIIII IIIIIII
651 TAACAGTAAGAAGTACGACTGCTGCGCGGAGATCTACCCCGATGTCACCT 700
201 AG..... 202
      |
701 ACTACTTTGTGATCCGGCGGCTGCCGCTGTTCTATACCATCAACCTCATC 750

```

FIGURE 7

07/938,154

(8 of 11)

SECTION A

1 .....CTGGCAGCAGAGGGCTGAGCACCGTCTATTTG 31  
 51 GATGCTGCTGCCAGCGGCCAGTGCCTCAGAAGCTGAGCACCGCCTGTTC 100  
 32 AGCGGCTGTTTGAAGATTACAATGAGATCATCCGGCCTGTAGCCAACGTG 81  
 101 AGTACCTGTTCTGAAGATTACAACGAGATCATCCGGCCAGTGGCTAATGTG 150  
 82 TCTGACCCAGTCATCATCCATTTCTGAGGTGTCCATGTCTCAGCTGGTGAA 131  
 151 TCCCATCCAGTCATCATCCAGTTTGAGGTGTCCATGTCTCAGCTGGTGAA 200  
 132 GGTGGATGAAGTAAACCGATCATGGAGACCAACCTGTGGCTCAAGCAA 181  
 201 GGTGGATGAAGTAAACCGATCATGGAAACCAACCTGTGGCTGAAGCAA 250  
 182 TCTGGAATGACTACAAGCTGAAGTGGAAACCCCTCTGACTATGGTGGGGCA 231  
 251 TCTGGAATGACTACAAGCTGAAATGGAAACCCCTCTGACTACCAAGGGGTG 300  
 232 GAGTTCATGCGTGTCCCTGCACAGAGATCTGGAAAGCCAGACATTGT... 278  
 301 GAGTTCATGCGTGTTCCTGCAGAGAGATCTGGAAACCAGACATCGTACT 350

.  
 .  
 .

SECTION B

1 .....TTCCAGGTGGACGACAAGACCAAGCCT 28  
 351 GTACAACAACGCTGATGGGGATTTCAGGTGGATGACAAGACCAAGCTC 400  
 29 TACTCAAGTACACTGGGGACGTGACTTGGATACCTCCGGCCATCTTTAG 78  
 401 TACTCAAGTACACAGGAGAAGTGACTTGGATCCCGCCGGCCATCTTTAG 450  
 79 AGCTCTGTAAAATCGACGTGACCTACTTCCCGTTTGATTACCAAAACTG 128  
 451 AGCTCATGCAAAATCGACGTGACCTACTTCCCATTCGACTACCAAAACTG 500  
 129 TACCATGAAGTTCGGTTCCTGGTCCTACGATAAGGCGAAAATCGATCTGG 178  
 501 CACCATGAAGTTCGGCTCCTGGTCCTACGACAAGGCAAAGATCGACCTGG 550  
 179 TCCTGATCGGCTCTTCCATGAACCTCAAGGACTATTGGGAGAGCGGCGAG 228  
 551 TCCTCATCGGCTCCTCCATGAACCTCAAGGACTACTGGGAGAGTGGCGAG 600  
 229 TGGGCCATCATCAAAGCCCCAGGCTACAAACACGACATCAAGTACAAGT 278  
 601 TGGGCTATCATTAAAGCCCCGGGCTACAAACATGAAATCAAGTACAAGT 650  
 279 CTGCGAGGAGATCTACCCCGACATCAC..... 305  
 651 CTGTGAGGAGATCTACCAAGACATCACGTAATCGCTGTACATCCGTGCGC 700



```

1  ATGCCCGCTGGCATGGCCGGCGCTGCGGCCCGTGGCGCTGCTCCTTGG 50
   |||| ||| |||||||| || || | | |||||||| |
1  ATGCTGGCTTGTCATGGCCGGGCACTCCAACCTCAATGGCGCTGTTC...AG 47

51  CTTGCGCCTCCTCCGGCTGTGCTCAGGGGTGTGGGGTACGGATACAGAGG 100
   |||| |||| || |||||||||||||| || || | | ||||||||
48  CTTCAGCCTTCTTTGGCTGTGCTCAGGGGTTTTGGGAAGTACACAGAGG 97

101 AGCGGCTGGTGGAGCATCTCCTGGATCCTTCCCGCTACAACAAGCTTATC 150
     |||||| |||||||||| || |||| |||||| |||||| ||
98  AGCGGCTAGTGGAGCATCTCTTAGATCCCTCCCGCTATAACAAGCTGATT 147

151 CGCCAGCCACCAATGGCTCTGAGCTGGTGACAGTACAGCTTATGGTGTC 200
     || |||| || || |||||||||||||| |||||| |||| ||
148 CGTCCAGCTACTAACGGCTCTGAGCTGGTGACTGTACAGCTCATGGTATC 197

201 ACTGGCCAGCTCATCAGTGTGCATGAGCGGGAGCAGATCATGACCACCA 250
     | |||| |||||| |||||| |||||| |||||| ||||||
198 ATTGGCTCAGCTCATTAGTGTGCACGAGCGGGAGCAGATCATGACCACCA 247

251 ATGTCTGGCTGACCCAGGAGTGGGAAGATTATCGCCTCACCTGGAAGCCT 300
     |||||||||||||||||| |||||| |||||| ||||||
248 ATGTCTGGCTGACCCAGGAGTGGGAAGATTACCGCCTCACATGGAAGCCT 297

301 GAAGAGTTTGACAACATGAAGAAAGTTCGGCTCCCTTCCAAACACATCTG 350
     || || || |||| |||||| |||||| |||||| ||||||
298 GAGGACTTCGACAATATGAAGAAAGTCCGGCTCCCTTCCAAACACATCTG 347

351 GCTCCAGATGTGGTCCTGTACAACAATGCTGACGGCATGTACGAGGTGT 400
     |||||||||| || |||||||||||||| |||||| || ||
348 GCTCCAGATGTGGTTCTATACAACAATGCTGACGGCATGTACGAAGTCT 397

401 CCTTCTATTCCAATGCCGTGGTCTCCTATGATGGCAGCATCTTCTGGCTG 450
     |||||||||| |||||| |||||| |||||| ||||||
398 CCTTCTATTCCAATGCTGTGGTCTCCTATGATGGCAGCATCTTTTGGCTA 447

451 CCGCCTGCCATCTACAAGAGTGCATGCAAGATTGAAGTAAAGCACTTCCC 500
     || |||||||||| ||||| |||||| || |||||| ||||
448 CCACCTGCCATCTACAAGAGTGCATGCAAGATTGAGGTGAAGCACTTCCC 497

501 ATTTGACCAGCAGAACTGCACCATGAAGTTCCGTTCGTGGACCTACGACC 550
     |||||||||| |||||| || || || |||||| ||||
498 ATTTGACCAGCAGAAATTGCACCATGAAGTTTCGCTCATGGACCTACGACC 547

551 GCACAGAGATCGACTTGGTGCTGAAGAGTGAGGTGGCCAGCCTGGACGAC 600
     | || |||| || |||||| || |||| |||||| ||||
548 GTA CTGAGATTGACCTGGTGCTCAAAAGTGATGTGGCCAGTCTGGATGAC 597

601 TTCACACCTAGTGGTGAGTGGGACATCGTGGCGCTGCCGGGCCGGGCAA 650
     |||||| || || |||||| || || |||| |||| ||||
598 TTCACACCCAGCCGGGAGTGGGACATCATCGCACTGCCAGGCCGACGCAA 647

651 CGAGAACCCCGACGACTCTACGTACGTGGACATCACGTATGACTTCATCA 700
     |||||| || || || |||||| || |||||| ||||
648 CGAGAACCCAGACGACTCCACCTATGTGGACATCACCTATGACTTCATCA 697

```

FIGURE 9(a)

FIGURE 9 (b)

07/938,154

1401 CTGGATCTTTGTCTTTGTCTGTGTCTTTGGCACCATCGGCATGTTCTGC 1430  
|||||  
1392 GTGGATCTTTGTCTTTGTCTGTGTCTTTGGGACCGTCGGCATGTTCTGC 1441  
1451 AGCCTCTCTTCCAGAACTACACCACCACCACCTTCCTCCACTCAGACCAC 1500  
|||||  
1442 AGCCTCTCTTCCAGAACTACACTGCCACTACCTTCCTCCACCCTGACCAC 1491  
1501 TCAGCCCCCAGCTCCAAGTGA 1521  
|||||  
1492 TCAGCTCCCAGCTCCAAGTGA 1512

FIGURE 9(c)